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#
library(downloader)
url="https://raw.githubusercontent.com/genomicsclass/dagdata/master/inst/extdata/msleep_ggplot2.csv"
filename <- basename(url)
download(url,filename)
library(dplyr)

#1 Read in the msleep_ggplot2.csv file with the function read.csv
#and use the function class to determine what type of object is returned.
dat <- read.csv(filename, header = TRUE)
class(dat)
#[1] "data.frame"

#2 Now use the filter function to select only the primates. How many animals in the table are primates?
#Hint: the nrow function gives you the number of rows of a data frame or matrix.
View(dat)
primates_data <- filter(dat, order %in% "Primates")
View(primates_data)
nrow(primates_data)
#[1] 12

#3 What is the class of the object you obtain after subsetting the table to only include primates?
class(primates_data)
#[1] "data.frame"


#4 Now use the select function to extract the sleep (total) for the primates. What class is this object?
#Hint: use %>% to pipe the results of the filter function to select.

primate_sleep <-
  filter(dat, order %in% "Primates") %>%
    select(sleep_total)
View(primate_sleep)
class(primate_sleep)
#[1] "data.frame"


#5 Now we want to calculate the average amount of sleep for primates (the average of the numbers computed above).
#One challenge is that the mean function requires a vector so, if we simply apply it to the output above,
#we get an error. Look at the help file for unlist and use it to compute the desired average.
mean(primate_sleep)
# warning message: argument is not numeric or logical: returning NA
?unlist
mean(unlist(primate_sleep))
#[1] 10.5


#6 For the last exercise, we could also use the dplyr summarize function.
#We have not introduced this function, but you can read the help file and repeat exercise 5,
#this time using just filter and summarize to get the answer.

filter(dat, order %in% "Primates") %>%
  summarize(ave_sleep = mean(sleep_total))
#   ave_sleep
#1      10.5

#or
primate_sleep %>%
  summarize(ave_sleep = mean(sleep_total))
#   ave_sleep
#1      10.5
```